SEQUENCE LISTING

(Onzinal aus OEB: 9.10.97)

1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Rotkreuzstiftung Zentrallaboratorium Blutspendedienst
- (B) STREET: Wankdorfstrasse 10

(C) CITY: Bern 22

(E) COUNTRY: Switzerland

(F) POSTAL CODE (ZIP): CH-3000

- (ii) TITLE OF INVENTION: Recombinant Fab-fragment with reactivity against Rhesus D antigens, DNA encoding them, complete antibodies comprising the Fab fragments and process for their preparation
- (iii) NUMBER OF SEQUENCES: 64
 - (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 - (v) CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP97/03253
 - (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP 96810421.6
 - (B) FILING DATE: 24-JUN-1996
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: Adult
 - (E) HAPLOTYPE: Diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA Library, LD1
 - (B) CLONE: LD1-40
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: Chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number

| • | (ix) | / 3 | TURE) NAI) LO | : ME/K CATI | EY: (ON:jo | CDR1 oin(| , CD1 | R2, 105, | CDR3 148 | 19 | 8, 2 | 95 | 342) | | | |
|------------------|------------------|-------------------|-----------------------|-------------------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|
| | (ix) | (A | | : ME/K CATI HER | ~ RT - 4 t | 27 | 5 ION: | /pro | duct | = "I | mmun | .oglo | buli | n, F | ab" | |
| | (xi) | SEQ | UENC | E DE | SCRI | PTIO | n: s | EQ I | D NO | : 1: | | | | | | • |
| AG In | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCT Ser | GGG Gly | GGA Gly | GGC Gly 10 | GTG Val | GTC Val | CAG Gln | CCT Pro | GGG Gly 15 | AGG Arg | 48 |
| cc er | CTG Leu | AGA Arg | CTC Leu 20 | TCC Ser | TGT Cys | ATA Ile | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | CTC Leu | AGG Arg 30 | AAT Asn | TAT Tyr | 96 |
| ;CC lla | ATG Met | CAC His | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCA Pro | GGC Gly | AAG Lys | GGG Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
| 3CA 1la | GGT Gly 50 | | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | AGT Ser | AAC Asn | AAA Lys | AAC Asn | TAT Tyr 60 | GCA Ala | GAC Asp | TCC Ser | GTG Val | 192 |
| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | ATC Ile 70 | TCC Ser | AGA Arg | GAC Asp | AAT Asn | TCC Ser 75 | AAG Lys | AAC Asn | ACG Thr | CTG Leu | TAT Tyr 80 | 240 |
| CTG Leu | CAA Gln | CTG Leu | AAC Asn | AGC Ser 85 | CTG Leu | AGA Arg | GAC Asp | GAG Glu | GAC Asp 90 | TILL | GCT Ala | GTG Val | TAT Tyr | TAT Tyr 95 | TGT Cys | 288 |
| GCG Ala | AGA Arg | GAG Glu | CGA Arg | Ala | GCA Ala | CGT Arg | GGT Gly | ATT Ile 105 | Ser | AGG Arg | TTC Phe | TAT Tyr | TAC Tyr 110 | - | ATG Met | 336 |
| GAC Asp | GTC Val | TGG Trp 115 | Gly | AAA Lys | GGG Gly | ACC Thr | ACG Thr 120 | vai | : ACC | GTC Val | : TCC Ser | CCA Pro 125 | | | | 375 |
| (2) | INF | ORMA | TION | FOR | SEQ | ID | NO: | 2: | | | | | | | | |
| | | (| (A) I (B) I | ENCE ENGT YPE: TOPOI | H: l' ami | .25 a .no a | umino acid | TICS aci | S: ids | | | | | | | |
| | (i: | i) Mo | OLECU EQUE | JLE I | YPE: ESCF | pro | oteir [ON: | sEQ | ID I | 10: | 2: | | | | | |
| : | n Vai | l Lys | s Lei | ı Lev | ı Glu | ı Sei | c Gly | y Gl | y Gly | y Va O | l Va | | | | y Arg 5 | |
| Sei | r Le | u Ar | g Let | u Sei 0 | c Cys | s Ile | e Ala | a Se | r Gl | y Ph | e Th | r Le | u Ar 3 | g As O | n Tyr | |
| Ala | a Me | t Hi: | s Trj 5 | p Va | l Ar | g Gl: | n Al | a Pr 0 | o Gl | у Lу | s Gl | y Le 4 | u Gl 5 | u Tr | p Val | |

la Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val 50 's Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr eu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys 90 la Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Met 105 sp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro 120 2) INFORMATION FOR SEQ ID NO: 3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 (B) CLONE: LD1-40 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..318 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION: join(64..96, 142..162, 259..288) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGC GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10 1

48

| TC | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AGC Ser | ATT Ile | AGG Arg | AGC Ser | CAT His 30 | TTG Leu | AAT Asn | 96 |
|-----------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| 'GG 'rp | TAT Tyr | CAG Gln 35 | CAG Gln | AAA Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AAG Lys | TTG Leu | CTG Leu 45 | ATC Ile | TAT Tyr | GGT Gly | 144 |
| ;CG :la | TCC Ser 50 | ACT Thr | TTG Leu | CAA Gln | AGT Ser | GGC Gly 55 | GTC Val | CCA Pro | TCA Ser | AGG Arg | TTC Phe 60 | AGT Ser | GGC Gly | AGT Ser | GGC Gly | 192 |
| CT Ser 65 | GGG Gly | GCA Ala | GTT Val | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | ATC Ile | GCC Ala | AGT Ser 75 | CTA Leu | CAA Gln | CCT Pro | GAA Glu | GAT Asp 80 | 240 |
| rTT ?he | GCA Ala | ACT Thr | TAC Tyr | TAC Tyr 85 | TGT Cys | CAA Gln | GAG Glu | AGT Ser | TAC Tyr 90 | AGT Ser | AAT Asn | CCT Pro | CTA Leu | ATC Ile 95 | ACC Thr | 288 |
| | GGC Gly | | | | | | | | | | | | | | | 318 |

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly 35 40 45

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr 85 90 95

Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys
100 105

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met

100

375

AC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCA sp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 115

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

In Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser 25 20

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 105 100

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 115

INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor

(D) DEVELOPMENTAL STAGE: Adult

(E) HAPLOTYPE: Diploid

(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

| · | • | (A (B |) CL | BRAR' | Y: c | DNA 1 | Libra | ary, | LD1 | | | | | | | |
|-----------------|------------------|------------------|------------------------|------------------------------|--------------|------------------|------------------|-------------------|------------------|------------|------------------|------------------|------------------|------------------|------------|-----|
| | iii) | (A |) CH) MA | N IN ROMO P PO ITS: | SOME SITI | /SEG | P 11 | | | some | 2 | | | | | |
| | (ix) | (A | | : ME/K CATI HER | ANT - 1 | 21 | 8 ION: | /pro | duct | = "I | mmun | .oglo | buli | n, F | ab" | |
| | (ix) | / A | TURE () NA () LC | : ME/K CATI | EY: ON:j | CDR1 oin(| , CD | R2, 96, | CDR3 | .162 | , 25 | 92 | 88) | | | |
| | (xi) | SEÇ | UENC | E DE | SCRI | PTIC | N: S | EQ I | D NO | : 7: | | | | | | |
| FTG /al 1 | | | | TCT Ser 5 | 003 | mcc | ሞሮሮ | CTG | ጥርጥ | GCA | TCT | GTA Val | GGA Gly | GAC Asp 15 | AGA Arg | 48 |
| FTC Val | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AAC Asn | ATT Ile | ATC Ile | CGC Arg | TAT Tyr 30 | TTA Leu | AAT Asn | 96 |
| IGG Irp | TAT Tyr | CAG Gln 35 | CAG Gln | AAG Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AGG Arg | CTC Leu | CTG Leu 45 | ATC Ile | TAT Tyr | GGT Gly | 144 |
| GCG Ala | TCC Ser 50 | ACT Thr | TTG Leu | CAA Gln | AGT Ser | GGG Gly 55 | GTC Val | CCA Pro | TCA Ser | AGG Arg | TTC Phe 60 | AGT Ser | GGC Gly | AGT Ser | GGA Gly | 192 |
| Ser 65 | Gly | Thr | Asp | | Thr 70 | Leu | Tnr | TTE | Ser | 75 | Дец | 02 | | | 80 | 240 |
| TTT Phe | GCA Ala | ACT Thr | TAC Tyr | TAC Tyr 85 | Cys | CAA Gln | CAG Gln | AGT Ser | TAC Tyr 90 | AL 9 | ACC Thr | CCT Pro | CCA Pro | TTC Phe 95 | ACT Thr | 288 |
| TTC Phe | GGC Gly | CCT Pro | GGG Gly 100 | ACC | AAA Lys | GTG Val | GAG Glu | ATC 1le 105 | г гус | | | | | | | 318 |
| (2) | INF | | | r FOR | | | | | • • | | | | | | | |
| | | (| A) I B) T | ENCE ENGT YPE: OPOI | H: 1 | lo6 a | umino acid | aci | lds | | | | | | | |
| | (xi | .) SI | EQUE | ICE I | ESCI | RIPT | [ON: | SEQ | | | | | | _ | | |
| 1 | _ | | | | 5 | | | | 1, | J | | | | | | |
| ۷al | Thi | : Ile | e Th: | r Cys | s Ar | g Ala | a Se | r Gli 2 | n Asi 5 | n Il | e Il | e Ar | g Ty: | r Lei 0 | u Asn | |

rp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly

la Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

er Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp

he Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr

he Gly Pro Gly Thr Lys Val Glu Ile Lys

- 2) INFORMATION FOR SEQ ID NO: 9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: Adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA LIBRARY, LD1
 - (B) CLONE: LD1-84
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: Chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(91..105, 148..198, 295..342)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...375
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 10 1

48

| cc | CTG Leu | AGA Arg | CTC Leu 20 | TCC Ser | TGT Cys | GAA Glu | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | CTC Leu | AGA Arg 30 | AGT Ser | TCT Ser | 96 |
|----------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|
| GC ly | ATG Met | CAC His 35 | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCT Pro | GGC Gly | AAG Lys | GGG Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
| CA la | CTT Leu 50 | ATA Ile | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | AGT Ser | ATC Ile | AGA Arg | TCG Ser | TAT Tyr 60 | GCA Ala | GAA Glu | TCC Ser | GTG Val | 192 |
| AG ys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | ATC Ile 70 | TCC Ser | AGA Arg | GAC Asp | ACT Thr | TCC Ser 75 | AAG Lys | AAC Asn | ACC Thr | CTA Leu | TAT Tyr 80 | 240 |
| TC eu | CAA Gln | ATG Met | CGC Arg | AGT Ser 85 | CTG Leu | AGT Ser | GCC Ala | GAC Asp | GAC Asp 90 | ACG Thr | GCT Ala | GTG Val | TAT Tyr | TAC Tyr 95 | TGT Cys | 288 |
| ;CG \la | AGA Arg | GAC Asp | AAG Lys 100 | GCG Ala | GTT Val | CGG Arg | GGA Gly | ATT Ile 105 | AGC Ser | AGG Arg | TAC Tyr | AAC Asn | TAT Tyr 110 | TAC Tyr | ATG Met | 336 |
| ;AC | GTC Val | TGG Trp 115 | GGC Gly | AAA Lys | GGG Gly | ACC Thr | ACG Thr 120 | GTC Val | ACC Thr | GTC Val | TCC Ser | TCA Ser 125 | | | | 375 |
| | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125

(2) INFORMATION FOR SEQ ID NO: 11:

| • | (1) | (A (B (C |) LEI) TYI) STI | NGTH: PE: 1 RANDI | 31! nucle EDNE: | baseic assistant | se pa acid sing: | | | | | | | | | |
|------------------|------------------|------------------|-------------------------|-------------------------|-----------------------------|---------------------------------------|------------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| | (ii) | MOL | ECUL | E TYI | PE: · | CDNA | to 1 | mRNA | | | | | | | | |
| (| iii) | HYP | OTHE' | rica: | L: N |) | | | | | | | | | | |
| e. | (iv) | ANT | I-SE | NSE: | ИО | | | | | | | | | | | , |
| | (v) | FRA | GMEN' | T TY | PE: | N-te | rmin | al | | | | | | | | |
| | (vi) | (A (C (D |) OR) IN) DE | DIVII VELO: PLOT | SM: DUAL PMEN YPE: | : Homo ISO TAL dip Per | LATE STAG loid | : Hy] E: A | peri: dult | | | | D do | nor | | |
| (| vii) | (A |) LI | TE S BRAR ONE: | Y: c | DNA | LIBR | ARY, | LD1 | | | | | | | |
| (∨ | iii) | (A |) CH | P PO | SOME SITI | OME: /SEG ON: omos | p11 | | | | 2 | | | | | |
| | (ix) | (A | I) TO | ME/K | ON : 1 | CDS 31 RMAT | 5 TON: | /pro | duct | = "I | mmun | oglo | buli | n, F | ab" | |
| | (ix) | (2 | TURE () NA () LC | ME/K | EY: ON:j | CDR1 oin(| , CI |)R2, 96, | CDR3 | .162 | 2, 25 | 92 | 85) | | | |
| | (xi) | SEÇ | UENC | E DE | SCRI | PTIC | N: S | SEQ I | D NC |): 11 | - : | | | | | |
| GTG Val 1 | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TCC Ser | CTG Leu | TCT Ser 10 | GCA Ala | TCT Ser | ATA Ile | GGA Gly | GAC Asp 15 | AGA Arg | 48 |
| GTC Val | ACC Thr | ATC Ile | ACC Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AGT Ser | ATC Ile | ATC Ile | AGG Arg | TAT Tyr 30 | TTG Leu | AAT Asn | 96 |
| TGG Trp | TAT Tyr | CAG Gln 35 | CAC His | AAA Lys | CCA Pro | GGA Gly | AAA Lys 40 | GCC Ala | CCT Pro | AAA Lys | CTC Leu | CTC Leu 45 | ATC Ile | TTT Phe | GCT Ala | 144 |
| GCA Ala | TCG Ser 50 | AAT Asn | TTG Leu | CAA Gln | ACT Thr | GGG Gly 55 | GTC Val | CCA Pro | TCC Ser | AGG Arg | TTC Phe 60 | AGT Ser | GGC Gly | AGT Ser | GGA Gly | 192 |
| TCT Ser 65 | GGG Gly | ACA Thr | GAT Asp | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | ATC Ile | AGT Ser | GAC Asp 75 | CTG Leu | CAG Gln | CCT Pro | GAG Glu | GAT Asp 80 | 240 |
| mm.c | CCA | х ст | መልሮ | ጥልሮ | ጥርጥ | CAA | CAG | AGT | TAC | AGT | AGG | CCG | TTC | ACT | TTT | 288 |

he Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe 85 90 95

GC CGG GGG ACC AGC CTG GAC ATC AAA ly Arg Gly Thr Ser Leu Asp Ile Lys 100 105 315

2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Tal Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe 85 90 95

Gly Arg Gly Thr Ser Leu Asp Ile Lys 100 105

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (V) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA LIBRARY, LD1

| | • | (B |) CL | ONE: | LD1 | -110 | | | | | | | | | • | |
|------------------|------------------|-------------------|------------------------|------------------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|
| ζv | iii) | (A |) CH | N IN ROMO P PO ITS: | SOME SITI | /SEGI | q32. | 3 | | | 14 | | | | | |
| | (ix) | (A | | : ME/K CATI HER | ANT . 1 | 27 | 5 ION: | /pro | duct | = "I | mmun | oglo | buli | n, F | ab" | |
| | (ix) | / 7 | TURE () NA () LC | : ME/K CATI | EY: ON:j | CDR1 oin(| , CD 91 | R2, 105, | CDR3 148 | 19 | 8, 2 | 95 | 348) | | | , |
| | (xi) | SEÇ | UENC | E DE | SCRI | PTIO | N: S | EQ I | D NO | : 13 | : | | | | | |
| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCT Ser | GGG Gly | GGA Gly | GGC Gly 10 | GTG Val | GTC Val | CAG Gln | CCT Pro | GGG Gly 15 | AGG Arg | 48 |
| TCC Ser | CTG Leu | AGA Arg | CTC Leu 20 | TCC Ser | TGT Cys | ATA Ile | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | CTC Leu | AGG Arg 30 | AAT Asn | TAT Tyr | 96 |
| GCC Ala | ATG Met | CAC His 35 | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCA Pro | GGC Gly | AAG Lys | GGG Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
| GCA Ala | GGT Gly 50 | ATA Ile | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | AGC Ser | AAC Asn | AAA Lys | AAC Asn | TAT Tyr 60 | GCA Ala | GAC Asp | TCC Ser | GTG Val | 192 |
| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | ATC Ile 70 | TCC Ser | AGA Arg | GAC Asp | AAC Asn | TCC Ser 75 | AAG Lys | AAC Asn | ACT Thr | CTG Leu | TTT Phe 80 | 240 |
| CTG Leu | CAC His | ATG Met | AAC Asn | AGC Ser 85 | CTG Leu | AGA Arg | GCC Ala | GAG Glu | GAC Asp 90 | TIIT | GCT Ala | ACA Thr | TAT Tyr | TAC Tyr 95 | - 4 | 288 |
| GCG Ala | AGA Arg | GAG Glu | AGG Arg 100 | Ala | ATT Ile | CGG Arg | GGA Gly | ATC Ile 105 | Ser | AGA Arg | TAC Tyr | AAT Asn | TAC Tyr 110 | TAC Tyr | ATG Met | 336 |
| GAC Asp | GTC Val | TGG Trp 115 | Gly | AAG Lys | GGG Gly | ACC Thr | ACG Thr 120 | val | ACC Thr | GTC Val | TCC Ser | TCA Ser 125 | | | | 375 |
| (2) | INF | ORMA | TION | FOR | SEQ | ID | ио: | 14: | | | | | | | | |
| | | (| A) I B) I | ENCE ENGT YPE: | H: 1 ami | .25 a .no a | minc cid | TICS aci | 3: Lds | | | | | | | |
| | (xi |) SE | EQUEN | ILE I | ESCF | RIPTI | ON: | SEQ | | | | | | | | |
| | ı Val | L Lys | s Lev | ı Lev | ı Glu | ı Sei | c Gly | 7 Gly | y Gly 10 | y Vai | L Val | L Glr | n Pro | 0 Gly | y Arg | |

Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe 65

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys

Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120

- (2) INFORMATION FOR SEQ ID NO: 15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: Adult
 - (E) HAPLOTYPE: Diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA Library, LD1
 - (B) CLONE: LD1-110
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: Chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: chromosome b.No
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...315
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(64..96, 142..162, 259..285)

| | (xi) | SEQ | UENC | E DE | SCRI | PTIC | N: S | EQ I | D NC | : 15 | : | | | | | |
|------------------|------------|------------------|-------------------|------------------------------|------------------|--------------|------------------|-------------------|------------------|------------------|------------|------------------|------------------|------------------|------------------|------------|
| GTG Val | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TCC Ser | CTG Leu | TCT Ser 10 | GCA Ala | TCT Ser | GTA Val | GGA Gly | GAC Asp 15 | Arg | 48 |
| GTC Val | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AGC Ser | ATT Ile | CGA Arg | AGC Ser | TCT Ser 30 | TTA Leu | AAT Asn | 96 |
| IGG Trp | TAT Tyr | CAG Gln 35 | CAG Gln | AAA Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AAA Lys | GTC Val | CTG Leu 45 | ATC Ile | TAT Tyr | GCT Ala | 144 |
| Ala | Ser 50 | Ser | Leu | Gln | Ser | 55 | Val | Pro | ser | Arg | 60 | Ser | Gry | ALG | GGA Gly | 192 |
| TCT Ser 65 | GGG Gly | ACA Thr | GAT Asp | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | ATC Ile | AGC Ser | AGT Ser 75 | CTG Leu | CAG Gln | CCT Pro | GAA Glu | GAT Asp 80 | 240 |
| TTT Phe | GCG Ala | ACT Thr | TAT Tyr | TAT Tyr 85 | TGT Cys | CAA Gln | CAG Gln | AGT Ser | TCC Ser 90 | Ser | TCC Ser | TCG Ser | TGG Trp | ACG Thr 95 | TTC Phe | 288 |
| GGC Gly | CAA Gln | GGG Gly | ACC Thr 100 | AAG Lys | GTG Val | GAA Glu | ATC Ile | AAA Lys 105 | | | | | | | | 315 |
| (2) | INF | ORMA' | TION | FOR | SEQ | ID | ио: | 16: | | | | | | | | |
| | | (| A) L B) T | ENCE ENGT YPE: OPOL | H: 1 ami | 05 a no a | cid | TICS aci | : ds | | | | | | | |
| | (ii (xi |) MO | LECU QUEN | LE T | YPE: ESCR | pro | tein | SEQ | ID N | 10: 1 | .6: | | | | | |
| Val | Met | | | | Pro | | | | | Ala | | · Val | L Gly | y Asy 1 | Arg | |
| Val | Thr | · Ile | Thr | | Arg | Ala | . Ser | Glr 25 | n Sei | : Ile | e Arg | g Sei | Sei 30 | r Lei | ı Asn | |
| Trp | туг | Gln 35 | | Lys | Pro | Gly | 7 Lys | s Ala | a Pro | D Lys | s Val | 1 Le: 4! | 1 Ile 5 | е Ту: | r Ala | |
| Ala | Ser 50 | | Leu | Gln | ser | Gly 55 | y V a: | l Pro | o Sei | r Ar | g Phe | e Sei | r Gl | y Ar | g Gly | |
| 65 | 5 | | | | 70 |) | | | | ′ | , | | | | u Asp 80 | |
| Ph€ | e Ala | a Thr | туг | Tyr 85 | Cys | s Gl | n Gl | n Se | r Se 9 | r Se O | r Se | r Se | r Tr | p Th 9 | r Phe 5 | |
| Gly | , Gli | n Gly | 7 Thi | Lys | va: | l Gl | u Il | e Ly 10 | s 5 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 17:

| • | (i) | (A) (B) | ENCE LENG TYP: STR. TOP | GTH: E: nu ANDEI | 378 ucle DNES | base ic ac S: s: | e par cid ingl | Irs | | | | | | | | |
|-----------------|------------|-------------------|--|-------------------------|---------------------|------------------------|----------------------|--------------|------------------|------------|------------|------------|------------|------------|------------|-----|
| (| ii) | MOLE | CULE | TYP | E: ˌc | DNA ' | to m | RNA | | | | | | | | |
| (i | ii) | нурс | THET | ICAL | : NO | ı | | | | | | | | | | |
| (| iv) | ANTI | -SEN | SE: | NO | | | | | | | | | | | |
| | (v) | FRAC | MENT | TYP | E: N | -ter | mina | .1 | | | | | | | | , |
| (| vi) | (A) (C) (D) | ORG ORG IND DEV HAF CEL | ANIS IVID ELOP | M: H UAL MENT | lomo ISOL AL S | ATE: TAGE oid | нур E: ad | luit | | | sus | D do | nor | | |
| (v | rii) | (A | EDIAT) LIE) CLC | BRARY | : CI |)NA I | JIBR# | ARY, | LD1 | | | | | | | |
| (vi | Lii) | (A | ITION) CHI) MAI) UNI | ROMOS | SOME, | /SEGN ON: 0 | 332 | 3 | | | 14 | | | | | |
| | | (A (B (D | TURE:) NAI) LOG) OTI | ME/KI CATIO HER : | ON:1 INFO | 378 RMAT | ION: | | | | mmun | oglo | buli | n, F | ab" | |
| | | (E |) NA | CATI | ON:j | oin(| 91 | 105, | 148 | 19 | | 95 | 345) | | | |
| | | | UENC | | | | | | | | | 01.0 | 00T | ccc | 7 7 G | 48 |
| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCA Ser | GGA Gly | GGA Gly | GGC Gly 10 | GTG Val | Val | Gln | Pro | Gly 15 | Lys | |
| TCC Ser | Leu | Arg | CTT Leu 20 | Ser | cys | Ala | Ala | 25 | GIY | FIIC | | | 30 | | | 96 |
| Gly | Met | His 35 | TGG Trp | Val | Arg | GIN | 40 | PLO | GIŞ | шу | 017 | 45 | | - | | 144 |
| Ala | Phe 50 | Ile | TGG Trp | Phe | Asp | 55 | Ser | ASII | цуз | -1- | 60 | | _ | | | 192 |
| Lys 65 | Gly | Arg | TTC Phe | Thr | 70 | Thr | Arg | Asp | ASII | 75 | 270 | | | | 80 | 240 |
| CTG Leu | CAA Gln | ATG Met | AAC Asn | AGC Ser | CTG Leu | AGA Arg | GCC Ala | GAG Glu | GAC Asp | ACG Thr | GCT Ala | GTC Val | TAT Tyr | TAC Tyr | TGT Cys | 288 |

CG AGA GAG ACC TCA GTA AGG CTA GGG TAT AGC CGC TAC AAT TAC TAC 336 la Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr 105 100 378 ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC ATC TCG TCA let Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser 120 115

90 .

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

31n Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr 105

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser 120 115

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor

| * | • | ÌΕ |) DE ;) HA ;) CE | PLOT | YPE: | dip | loid | | | | te B | | | | | |
|------------------|------------------|------------------|---------------------------------|----------------------|--------------------|----------------------|---------------------|-------------------|------------------|------------------|------------|------------------|------------------|------------------|------------------|-----|
| (| vii) | (A | EDIA) LI 3) CL | BRAR | Y: c | DNA | LIBR | ARY, | LD1 | | | | | | | |
| (v | riii) | (A | ITIC () CH () MA () UN | ROMO P PO | SOME | SSEG | MENT p11 | | | | : 2 | | | | | , |
| | (ix) | (A | TURE L) NA B) LC | ME/K | ON: 1 | 31 | .8 'ION: | /pro | oduct | := "I | mmun | oglc | buli | .n, F | 'ab" | |
| | (ix) | (A | TURE 1) NA 3) LC | ME/K | EY: ON:j | CDR1 | , CI | DR2, | CDR3 | .162 | 2, 25 | 592 | 188) | | | |
| | (xi) | SEÇ | QUENC | E DE | ESCRI | PTIC | n: s | SEQ 1 | D NC |): 19 |): | | | | | |
| GTG Val 1 | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TCC Ser | CTG Leu | TCT Ser 10 | GCA Ala | TCT Ser | GTA Val | GGA Gly | GAC Asp 15 | AGA Arg | 48 |
| GTC Val | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AGC Ser | ATT Ile | AGG Arg | AGC Ser | CAT His 30 | TTG Leu | AAT Asn | 96 |
| TGG Trp | TAT Tyr | CAG Gln 35 | CAG Gln | AAA Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AAG Lys | CTC Leu | CTG Leu 45 | ATC Ile | TAT Tyr | GCT Ala | 144 |
| GCA Ala | TCC Ser 50 | AGT Ser | TTG Leu | CAA Gln | GGT Gly | GGG Gly 55 | GTC Val | CCA Pro | Ser | AGG Arg | Pne | Ser | GGC Gly | AGT Ser | GGA Gly | 192 |
| TCT Ser 65 | GGG Gly | ACA Thr | GAT Asp | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | ATC Ile | AGC Ser | AGT Ser 75 | CTG Leu | CAA Gln | CCT Pro | GAA Glu | GAT Asp 80 | 240 |
| TTT Phe | GCA Ala | ACT Thr | TAT Tyr | TAC Tyr 85 | TGT Cys | CAA Gln | CAG Gln | AGT Ser | TAC Tyr 90 | AGG Arg | GCC Ala | CCT Pro | CAG Gln | TGG Trp 95 | ACG Thr | 288 |
| TTC Phe | GGC Gly | CAA Gln | GGG Gly 100 | ACC Thr | AAG Lys | GTG Val | GAA Glu | ATC Ile 105 | Lys | | | | | | | 318 |
| (2) | INF | ORMA' | TION | FOR | SEQ | ID : | NO: | 20: | | | | | | | | |
| | | (i) (. | SEQU A) L B) T | ENCE ENGT YPE: | CHA H: 1 ami | RACT 06 a no a | ERIS mino cid | TICS | : ds | | | | | | | |

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala

Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA LIBRARY, LD2
 - (B) CLONE: LD2-1
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...375
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(91..105, 148..198, 295..342)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCT Ser | GGG Gly | GGA Gly | GGC Gly 10 | GTG Val | GTC Val | CAG Gln | CCG Pro | GGG Gly 15 | GGG Gly | 48 |
|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|
| rcc Ser | CTG Leu | AGA Arg | CTC Leu 20 | TCC Ser | TGT Cys | GTA Val | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | CTC Leu | AGG Arg 30 | AGT Ser | TAT Tyr | 96 |
| GGC Gly | ATG Met | CAC His 35 | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCA Pro | GGC Gly | AAG Lys | GGC Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
| GCT Ala | TTT Phe 50 | ATA Ile | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | AGT Ser | AAT Asn | AAA Lys | GGA Gly | TAT Tyr 60 | GTA Val | GAC Asp | TCC Ser | GTG Val | 192 |
| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | ATC Ile 70 | TCC Ser | CGA Arg | GAC Asp | AAT Asn | TCC Ser 75 | AAG Lys | AAC Asn | ATG Met | GTC Val | TAT Tyr 80 | 240 |
| CTG Leu | CAA Gln | ATG Met | AAC Asn | AGC Ser 85 | CTG Leu | AGA Arg | GCC Ala | GAT Asp | GAC Asp 90 | ACG Thr | GCT Ala | GTA Val | TAT Tyr | TAT Tyr 95 | TGT Cys | 288 |
| GCG Ala | AGA Arg | GAG Glu | AAG Lys 100 | GCG Ala | CTT Leu | CGG Arg | GGA Gly | ATC Ile 105 | Ser | AGA Arg | TAC Tyr | AAC Asn | TAT Tyr 110 | -1- | CTG Leu | 336 |
| GAC Asp | GTC Val | TGG Trp 115 | GGC Gly | AAG Lys | GGG Gly | ACC Thr | ACG Thr 120 | vaı | ACC | GTC Val | TCC Ser | TCA Ser 125 | | | | 375 |
| | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 65 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

| Y . | la Arģ | | ys Ala 00 | Leu Ar | g Gly | Ile 105 | Ser i | Arg 1 | Tyr i | Asn : | Tyr 1 | Cyr I | eu | | |
|------------|--------------------|--------------------------|--|-------------------------------------|--|---------------------|------------------|------------|------------|------------------|------------------|------------------|------------|-----|---|
| ¥: | sp Val | Trp G: 115 | ly Lys | Gly Th | r Thr 120 | Val | Thr ' | Val S | Ser | Ser 125 | | | | | |
| (: | 2) INFO | RMATI | ON FOR | SEQ II | NO: 2 | 23: | | | | | | | | | |
| | | (A) (B) (C) (D) | ENCE CH LENGTH TYPE: STRANI TOPOLO | : 333 nucle: EDNESS GY: 1: | base place place in a circular place | oairs l gle | | | | | | | | | |
| | (ii) | MOLE | CULE TY | PE: cl | ONA to | mRNA | | | | | | | | | |
| | (iii) | НУРО | THETICA | AL: NO | | | | | | | | | | | |
| | (iv) | ANTI | -sense: | NO | | | | | | | | | | | |
| | (v) | FRAG | MENT T | PE: N | -termin | nal | | | | | | | | | |
| | (vi) | (A) (C) (D) | INAL SO ORGANI INDIVI DEVELO HAPLO CELL | ISM: HODAL OPMENT | ISOLATI AL STAC diploic | E: Hy GE: a d | peri | | | | Dα | onor | | | |
| | (vii) | (A) | DIATE S LIBRAI CLONE | RY: cD | NA LIB | RARY, | LD2 | : | | | | | | | |
| | (viii) | (A) (B) | TION II CHROMO MAP PO UNITS | OSOME/ OSITIO | SEGMEN' N: q11 | | | | 22 | | | | | | |
| | (ix) | (R) | TURE: NAME/I LOCAT OTHER | TON: 1. | .333 | :/pro | oduct | := "I | mmur | noglo | buli | .n, F | 'ab" | | |
| | | (B) | NAME/ LOCAT | ION:jo | in(61. | .99, | 145 | 165 | | 522 | 294) | | | | |
| | | | JENCE D | | | | | | | | | | | 4.0 | |
| 7 | TG GTG al Val | ACT C | CAG CCA Sln Pro 5 | Pro S | CA GCG er Ala | TCT Ser | GGG Gly 10 | ACC | Pro | GGA | Gln | AGG Arg 15 | Val | 48 | |
| 7 | ACC ATC Thr Ile | TCT 1 | TGT TCT Cys Ser 20 | GGA A | GC AAC Ser Asn | TCC Ser 25 | Ile | CTT Leu | GGA Gly | AGT Ser | AAG Lys 30 | TAT Tyr | GTA Val | 96 | ı |
| j | TAC TGG Tyr Trp | TAC (Tyr (| CAG AAA Gln Lys | CTC (| CCA GGA Pro Gly 40 | Thr | GCC Ala | CCC Pro | AAA Lys | CTC Leu 45 | CTC Leu | ATC Ile | TAT Tyr | 144 | f |
| 1 | AAG AAT | GAT (| CAG CGG | CCC T | CA GGG Ser Gly | GTC Val | TCT | GAC Asp | CGA Arg | TTC Phe | TCT Ser | GGC Gly | TCC Ser | 192 | ! |

| AAG Lys 65 | TCT Ser | GGC Gly | ACC Thr | TCG Ser | GCC Ala 70 | TCC Ser | CTG Leu | GCC Ala | ATC Ile | AGT Ser 75 | GGG Gly | CTC Leu | CGG Arg | TCC Ser | GAG Glu 80 | |
|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|--|
|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|--|

288

240

GAT GAG GCT GAC TAT TAC TGT GCA CCA TGG GAT GCC AAC CTG GGT GGC Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly 85

200

CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 100 105 110

55

333

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val

Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val 20 25 30

Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr 35 40 45

Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser 50 60

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly 95

Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homo sapiens

| • | • | (D) | DEV HAF | ELOP | MENI | AL S dinl | TAGE oid | : ad | luit | ocyt | e B | | | | | |
|------------------|------------------|-------------------|----------------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|
| (V | ii) | (A) | EDIAT) LIE) CLO | BRARY | C: CL |)NA I | Libra | ary, | LD2 | | | | | | | |
| iv) | Lii) | (A) | ITION CHI MAN UNI | ROMOS | SOME, | ON: (| 332 | 3 | | | 14 | | | | | , |
| , | (ix) | (A | TURE) NAI) LOG) OT | ME/K | | | 5 ION: | /pro | duct: | = "I1 | mmun | oglok | ouli | n, Fa | ab" | |
| | (ix) | | TURE) NA) LO | 34T3 / TZ | EY: ON:j | CDR1 oin(| , CD 91 | R2, 105, | CDR3 148 | 19 | 8, 2 | 95: | 342) | | | |
| | (xi) | SEQ | UENC | E DE | SCRI | PTIO | N: S | EQ I | D NO | : 25 | : | | | | | |
| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCG Ser | GGG Gly | GGA Gly | GGC Gly 10 | GTG Val | GTC Val | CAG Gln | CCG Pro | GGG Gly 15 | GGG Gly | 48 |
| TCC Ser | CTG Leu | AGA Arg | CTC Leu 20 | TCC Ser | TGT Cys | GAA Glu | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | CTC Leu | AGA Arg 30 | AGT Ser | TCT Ser | 96 |
| GGC Gly | ATG Met | CAC His | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCT Pro | GGC Gly | AAG Lys | GGG Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
| GCA Ala | CTT Leu 50 | ATA Ile | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | AGT Ser | ATC Ile | Arg | TCG Ser | TAT Tyr 60 | GCA Ala | GAA Glu | TCC Ser | GTG Val | 192 |
| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | ATC Ile 70 | ser | AGA Arg | GAC Asp | ACT Thr | TCC Ser 75 | AAG Lys | AAC Asn | ACC Thr | CTA Leu | TAT Tyr 80 | 240 |
| CTC Leu | CAA Gln | ATG Met | CGC Arg | AGT Ser 85 | Leu | AGT Ser | GCC Ala | GAC Asp | GAC Asp 90 | | GCT Ala | GTG Val | TAT Tyr | TAC Tyr 95 | TGT Cys | 288 |
| GCG Ala | AGA Arg | GAC Asp | AAG Lys | Ala | GTT Val | CGG Arg | GGA Gly | ATT Ile | Jer | AGG Arg | TAC | AAC Asn | TAT Tyr 110 | TAC | ATG Met | 336 |
| GAC Asp | GTC Val | TGG Trp 115 | Gly | : AAA 'Lys | GGG Gly | ; ACC | Thr | . val | ACC Thr | GTC Val | TCC Sei | TCA Ser 125 | · · | | | 375 |
| (2) | INE | ORMA | (OIT | ı FOF | R SEC | Q ID | NO: | 26: | | | | | | | | |
| | | (i) | SEQU (A) I (B) I | JENCI LENGT | E CHI | ARAC' | rERIS amin | STICS | s: ids | | | | | | | |

(C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125

- (2) INFORMATION FOR SEQ ID NO: 27:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-4
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...312

| | | (D |) OT | HER | INFO | RMAT | ION: | /pro | duct | = "I | mmun | oglo | buli | n, F | ab" | |
|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| • | (ix) | / A | 1 NA | MF/K | EY: ON:j | CDR1 oin(| , CD | R2, 96, | CDR3 | .162 | , 25 | 92 | 82) | | | |
| | (xi) | SEQ | UENC | E DE | SCRI | PTIO | n: s | EQ I | D NO | : 27 | : | | | | | |
| TG /al 1 | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TCC Ser | CTG Leu | TCT Ser 10 | GCA Ala | TCT Ser | GTA Val | GGA Gly | GAC Asp 15 | AGA Arg | 48 |
| FTC /al | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | ACA Thr | AGT Ser | CAG Gln 25 | ACC Thr | ATT Ile | AGC Ser | AGA Arg | AAT Asn 30 | TTA Leu | AAT Asn | 96 |
| rgg Irp | TAT Tyr | CAG Gln 35 | CAG Gln | AAA Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AAG Lys | CTC Leu | CTG Leu 45 | ATC Ile | TAT Tyr | GCT Ala | 144 |
| ACA Thr | TCC Ser 50 | AGT Ser | TTG Leu | CAA Gln | AGT Ser | GGG Gly 55 | GTC Val | CCA Pro | TCA Ser | AGG Arg | TTC Phe 60 | AGT Ser | GGC Gly | AGT Ser | GGA Gly | 192 |
| rcT Ser 65 | GGG Gly | ACA Thr | GAT Asp | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | ATC Ile | AAT Asn | AGT Ser 75 | CTA Leu | CAA Gln | CCT Pro | GAA Glu | GAT Asp 80 | 240 |
| rrr Phe | GCA Ala | ACT Thr | TAC Tyr | TAC Tyr 85 | TGT Cys | CAA Gln | CAG Gln | AGT Ser | TAC Tyr 90 | ACT Thr | ACC Thr | CCT Pro | TCG Ser | TTC Phe 95 | GLI | 288 |
| CAA Gln | GGG Gly | ACC Thr | AAG Lys 100 | GTG Val | GAA Glu | ATC Ile | AAA Lys | | | | | | | | | 312 |
| (2) | | (i) | SEQU A) L | ENCE ENGT | CHA H: 1 | ID RACT | ERIS mino | rics | : ds | | | | | | | |
| | | • | B) T D) T | YPE: OPOL | ami OGY: | no a lin | cıd ear | | | | | | | | | |
| | (xi |) SE | QUEN | CE D | ESCR | pro IPTI | ON: | | | | | | | | | |
| Val | | Thr | Gln | Ser 5 | | Ser | Ser | Leu | Ser 10 | Ala | Ser | · Val | Gly | Asp 15 | Arg | |
| Val | Thr | Ile | Thr 20 | Cys | Arg | Thr | Ser | Gln 25 | Thr | · Ile | Ser | Arg | Asr 30 | ı Lev | a Asn | |
| Trp | Tyr | Gln 35 | | Lys | Pro | Gly | Lys 40 | Ala | Pro | Lys | Lev | Let 45 | ı Ile | ∋ Туі | r Ala | |
| Thr | Ser 50 | | Lev | Gln | Ser | Gly 55 | Val | Pro | Ser | Arg | Phe 60 | e Sei | Gly | y Sei | r Gly | |
| Ser 65 | | . Thr | . Ast | Phe | Thr. 70 | Leu) | Thr | Ile | e Asr | n Ser 75 | : Lev | ı Glı | n Pro | o Gl | u Asp 80 | |
| Ph€ | a Ala | Thr | туг | . Tyr | Cys | s Glr | Gln | Ser | ту1 | Thi | Thi | r Pro | o Se | r Ph | e Gly | |

95

Gln Gly Thr Lys Val Glu Ile Lys 100

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:

 - (A) ORGANISM: homo sapiens
 (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 (D) DEVELOPMENTAL STAGE: adult

 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-4
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 2
 - (B) MAP POSITION: pll
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...375
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(91..105, 148..198, 295..342)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCT Ser | GGG Gly | GGA Gly | GGC Gly 10 | TTG Leu | GTC Val | CAG Gln | CCG Pro | GGG Gly 15 | GGG Gly | 48 | |
|-----------------|------------|------------|------------|-----------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|-----|--|
| | | | | | | | | | | | | | | | | 0.0 | |

| TCC Ser | CTG Leu | AGA Arg | CTC Leu 20 | TCC Ser | TGT Cys | GTA Val | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | TTC Phe | AGG Arg 30 | AGT Ser | TAT Tyr | 96 |
|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|----|
|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|----|

| GGC Gly | ATG Met | CAC His | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCA Pro | GGC Gly | AAG Lys | GGC Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
|------------|------------|------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|-----|

| | _ | 35 | | | | | 40 | | | | | | | | | | |
|--------|------------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|-----|---|
| G A | CT TTT la Phe 50 | ATA Ile | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | AGT Ser | AAT Asn | AAA Lys | GGA Gly | TAT Tyr 60 | GTA Val | GAC Asp | TCC Ser | GTG Val | 192 | 2 |

| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | ATC Ile 70 | TCC Ser | CGA Arg | GAC Asp | AAT Asn | TCC Ser 75 | AAG Lys | AAC Asn | ATG Met | CTC Leu | TAT Tyr 80 | 240 |
|------------------|------------|-------------------|-------------------|------------------|------------------|------------|-------------------|-------------------|------------------|------------------|------------|-------------------|-------------------|------------------|------------------|-----|
| CTG Leu | CAA Gln | ATG Met | AAT Asn | AGC Ser 85 | CTG Leu | AGA Arg | GCC Ala | GAG Glu | GAC Asp 90 | ACG Thr | GCT Ala | GTA Val | TAT Tyr | TAT Tyr 95 | TGT Cys | 288 |
| GCG Ala | AGA Arg | Glu | AAG Lys 100 | GCG Ala | CTT Leu | CGG Arg | GGA Gly | ATC Ile 105 | AGT Ser | AGA Arg | TAC Tyr | AAC Asn | TAT Tyr 110 | TAC Tyr | CTG Leu | 336 |
| GAC Asp | GTC Val | TGG Trp 115 | GGC Gly | AAG Lys | GGG Gly | GCC Ala | ACG Thr 120 | GTC Val | ACC Thr | GTC Val | TCC Ser | TCA Ser 125 | | | | 375 |

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gln Val Lys Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110

Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser 115 120 125

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO

| | (v) | FRAG | MENT | TYP | E: N | -ter | mina | 1 | • | | | | | | | |
|------------------|------------------|-------------------|----------------------|---|---------------------|----------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| . (| vi) | (A) (C) (D) | ORG IND DEV | SOU SANIS DIVIE VELOFY PLOTY LL TY | M: H UAL MENT | Iomo ISOI AL S | LATE: STAGE | hyr ac | iuit | | | esus | D do | onor | | |
| (7 | vii) | (A) |) LIE | re so Brary One: | : cl | . ממכ | libra | ary. | LD2 | | | | | | | |
| (vi | Lii) | (A) |) CHI | N IN ROMOS P POS ITS: | SOME, | /SEGI ON: 1 | p11 | | | | 2 | | | | | |
| 1 | (ix) | (A | | : ME/KI CATION HER | | 2 1 | 8 ION: | /pro | duct | = "I | mmun | oglo | buli | n, F | ab" | |
| | (ix) | / 3 | TURE) NA) LO | : ME/K CATI | EY: ON:j | CDR1 oin(| , CD | R2, 96, | CDR3 | .162 | , 25 | 92 | 88) | | | |
| | | | | E DE | | | | | | | | | | | | |
| GTG Val | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TCC Ser | CTG Leu | TCT Ser 10 | GCA Ala | TCT Ser | ATA Ile | GGC Gly | GAC Asp 15 | AGA Arg | 48 |
| GTC Val | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AGC Ser | GTT Val | ACC Thr | AGG Arg | TCT Ser 30 | TTA Leu | AAT Asn | 96 |
| TGG Trp | TAT Tyr | CAG Gln 35 | CAG Gln | AAA Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AGG Arg | CTC Leu | CTA Leu 45 | ATC Ile | TTT Phe | GCT Ala | 144 |
| GCG Ala | TCC Ser 50 | ACT Thr | TTG Leu | CAA Gln | AGT Ser | GGG Gly 55 | GTC Val | CCA Pro | TCA Ser | AGG Arg | TTC Phe 60 | AGT Ser | GGC Gly | AGT Ser | GGA Gly | 192 |
| TCT Ser 65 | GGG Gly | ACA Thr | GAT Asp | TTC Phe | ACC Thr 70 | CTC Leu | ACC Thr | ATC Ile | AGC Ser | AGT Ser 75 | Dea | CAA Gln | CCT Pro | GAG Glu | GAT Asp 80 | 240 |
| TTT Phe | GGA Gly | ACT Thr | TAC Tyr | TAC Tyr 85 | TGT Cys | CAA Gln | CAG Gln | AAT Asn | TAC Tyr 90 | ALG | ACC Thr | CCT Pro | CAG Gln | TGG Trp 95 | ACG Thr | 288 |
| TTC Phe | GGC Gly | CAA Gln | GGG Gly 100 | ACC Thr | AAG Lys | GTA Val | GAA Glu | ATC Ile 105 | пyэ | • | | | | | | 318 |
| | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 106 amino acids(B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg 5

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 70 65

Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 90

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-10
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...378
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
 - (ix) FEATURE:

| (A) | NAME/KEY: | CDR1, | CDR2, | CDR3 |
|-------------|-----------|-------|-------|-------|
| \ / | | | 105 | 3 4 0 |

(B) LOCATION: join(91..105, 148..198, 298..345)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

| | | | UENC | | | | | | | | | | | | | |
|-----------|----------------------|------------|-------------------|-------------------|------------|------------------|-------------------|-------------------|-------------------|------------|------------------|-------------------|-------------------|-------------------|------------|-----|
| Glr 1 | | Lys | Leu | Leu 5 | GIU | ser | GIY | âră | 10 | , | | | | 15 | • | 48 |
| Sei | CTG Leu | Arg | Leu 20 | ser | Cys | vaı | Ата | 25 | GIJ | 1110 | | | 30 | | | 96 |
| GG Gl | C ATG Y Met | CAC His | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCA Pro | GGC Gly | AAG Lys | GGC Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
| GC' Al | r TTT a Phe 50 | ATA Ile | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | AGT Ser | AAT Asn | AAA Lys | GGA Gly | TAT Tyr 60 | GTA Val | GAC Asp | TCC Ser | GTG Val | 192 |
| AA Ly | G GGC s Gly | CGA Arg | TTC Phe | ACC Thr 175 | TTE | TCC Ser | CGA Arg | GAC Asp | AAT Asn 180 | TCC Ser | AAG Lys | AAC Asn | ATG Met | GTC Val 185 | TAT Tyr | 240 |
| CT Le | G CAA u Gln | ATG Met | AAC Asn | AGC Ser 85 | Leu | AGA Arg | GCC Ala | GAT Asp | GAC Asp 90 | | GCT Ala | GTA Val | TAT Tyr | TAT Tyr 95 | TAT | 288 |
| TG Cy | T GCG | AGA Arg | GAG Glu 100 | Lys | GCG Ala | CTI Leu | CGG Arg | GGA Gly 105 | 110 | AGC Ser | AGA Arg | TAC Tyr | AAC Asn 110 | TAT Tyr | TAC | 336 |
| C'I Le | G GAC eu Asp | GTC Val | Trp | GGC Gly | AAG Lys | GGG Gly | ACC Thr 120 | | GTC Val | C ACC | GTC Val | TCC Ser 125 | TCA Ser | <u>.</u> | | 378 |

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
- Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1
- Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
- Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35
- Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
- Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr

| | | | | 85 | | | | | 90 | | | | | ,,, | | | | |
|------------|------------|-------------------|---|---------------------|------------------------------|-----------------------------|----------------------|------------------|---------------|---------------------|----------------|------------|----------------|---------------------|--------------|------------|----|---|
| :ys i | Ala A | Arg (| 3lu L LOO | ys | Ala | Leu | Arg | Gly 105 | Ile | Ser | Arg | Tyr | Asn 110 | Tyr | Tyr | • | | |
| ieu i | Asp ' | Val 7 | rp G | ly | Lys _, | Gly | Thr 120 | Thr | Val | Thr | Val | Ser 125 | Ser | | | | | |
| (2) | INFO | RMAT: | ION F | FOR | SEQ | ID N | io: : | 35: | | | | | | | | | | |
| | (i) | (A) (B) (C) | UENCE) LEN) TYE) STE) TOE | IGTH PE: RAND | nuc DEDNI | 33 ba Leic ESS: | se] acio sino | paır 1 | S | | | | | | | | • | |
| | • | | ECULI | | | | A to | mRN | Ά | | | | | | | | | |
| (| | | OTHE | | | МО | | | | | | | | | | | | |
| | • | | I-SE | | | | ě | | | | | | | | | | | |
| | | | GMEN' | | | | ermi | nal | | | | | | | | | | |
| | (vi) | (A (C (D | GINAL ORC INITION | GAN DIV: VELO | ISM: IDUA OPME TYPE | Hom L IS NTAL : di | OLAT STA oloi | E: r GE: d | adu] | LC | | | ıs D | dono | or | | | |
| (| (vii) | (A | EDIA () LI () CL | BRA | RY: | CDNA | lik | rary | y, Ll | D2 | | | | | | | | |
| (7 | viii) | (P | SITIO A) CH B) MA C) UN | ROM | OSOM OSTI | E/SE | GMEN al: | L | | | | 2 | | | | | | |
| | (ix) | (2 | ATURE A) NA B) LC O) OI | ME/ | TONT . | . 1 . | 22 | q\:P | rodu | ct= | "Imm | unog | lobu | lin, | Fal | o " | | |
| | (ix | / 1 | ATURE A) NA B) LO | ME / | KEY: | : CDI | R1, 1(61 | CDR2 10 | , CD 2, 1 | R3 .48 | 168, | 265 | 29 | 4) | | | | |
| | - | | QUENC | | | | | | | | | | | | | | | _ |
| GTG Val | Val | ACT Thr | CAG Gln | Glu | CC Pr | C TC | A CT r Le | G AC u Th | II. Vo | TG TC 1 Se 10 | c cc r Pr | A GG | A GG y Gl | G AC y Th | A G' Ar V | TC al | 4 | 8 |
| ACT Thr | CTC Leu | ACC Thr | TGT Cys 20 | GCT Ala | T TC a Se | C AG r Se | C AC | r G | G GC Ly Al | CA GT La Va | C AC | C AC | . 9 | T TA Ly Ty 30 | AC T | AT Yr | 9 | 6 |
| CCA Pro | AAC Asn | TGG | TTC Phe | CA(| G CA n Gl | G AA n Ly | s Pr | T GC | GA CA | AA GO ln Al | CA CO La Pi | . O A | GG GG CG A: | CA CT La Le | rg A eu I | TT le | 14 | 4 |

| TAT Tyr | AGT Ser 50 | ACA Thr | AAC Asn | AAA Lys | AAA Lys | CAC His 55 | TCC Ser | TGG Trp | ACC Thr | CCT Pro | GCC Ala 60 | Arg | TTC Phe | TCA Ser | GGC | 192 |
|------------------|------------------|------------|-------------------|------------------|------------------|------------------|------------|-------------------|------------------|------------------|------------------|------------|-------------------|------------------|------------------|-----|
| TCC Ser 65 | Leu | CTT Leu | GGG Gly | GGC Gly | AAA Lys 70 | GCT Ala | GCC Ala | CTG Leu | ACA Thr | CTG Leu 75 | TCA Ser | GGT Gly | GTG Val | CAG Gln | CCT Pro 80 | 240 |
| GAA Glu | GAC Asp | GAG Glu | GCT Ala | GAA Glu 85 | TAT Tyr | TAC Tyr | TGC Cys | CTG Leu | CTC Leu 90 | TAC Tyr | TAT Tyr | GGT Gly | GGT Gly | GCT Ala 95 | CAA Gln | 288 |
| CTC Leu | GTA Val | TTC Phe | GGC Gly 100 | GGA Gly | GGG Gly | ACC Thr | AAG Lys | CTG Leu 105 | ACC Thr | GTC Val | CTA Leu | CGT Arg | CAG Gln 110 | CCC Pro | | 333 |

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
- Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val 1 5 10 15
- Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr 20 25 30
- Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile 35 40 45
- Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly
 50 55 60
- Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro 65 70 75 80
- Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln 85 90 95
- Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal

| . (| (vi) | ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B | | | | | | | | | | | | | | | |
|------------------|------------------|--|--|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|--|
| 7) | /ii) | (A | IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-11 | | | | | | | | | | | | | | |
| (v: | iii) | (A | POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number | | | | | | | | | | | | | | |
| | (ix) | (A) NAME/KEY: CDS (B) LOCATION:1375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" | | | | | | | | | | | | | | | |
| | | (A (B |) LO | ME/K CATI | ом: ј | oin(| , CD 91 | 105, | 148 | 19 | | 95 | 342) | | | | |
| | | | | | | | N: S | | | | | | | | | | |
| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCG Ser | GGG Gly | GIY | GGC Gly O | GTG Val | GTC Val | CAG Gln | LLO | GGG Gly .5 | GGG Gly | 48 | |
| TCC Ser | CTG Leu | AGA Arg | CTC Leu 20 | TCC Ser | TGT Cys | GAA Glu | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | CTC Leu | AGA Arg 30 | AGT Ser | TCT Ser | 96 | |
| GGC Gly | ATG Met | CAC His 35 | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCT Pro | GGC Gly | AAG Lys | GGG Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 | |
| GCA Ala | CTT Leu 50 | ATA Ile | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | AGT Ser | ATC Ile | AGA Arg | TCG Ser | TAT Tyr 60 | GCA Ala | GAA Glu | TCC Ser | GTG Val | 192 | |
| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | ATC Ile 70 | TCC Ser | AGA Arg | GAC Asp | ACT Thr | TCC Ser 75 | AAG Lys | AAC Asn | ACC Thr | CTA Leu | TAT Tyr 80 | 240 | |
| CTC Leu | CAA Gln | ATG Met | CGC Arg | AGT Ser 85 | CTG Leu | AGT Ser | GCC Ala | GAC Asp | GAC Asp 90 | TIII | GCT Ala | GTG Val | TAT Tyr | TAC Tyr 95 | TGT Cys | 288 | |
| GCG Ala | AGA Arg | GAC Asp | AAG Lys 100 | Ala | GTT Val | CGG Arg | GGA Gly | ATT Ile 105 | Ser | AGG Arg | TAC Tyr | AAC Asn | TAT Tyr 110 | -1- | ATG Met | 336 | |
| GAC Asp | GTC Val | TGG Trp 115 | Gly | AAA Lys | GGG Gly | ACC Thr | ACG Thr 120 | val | ACC Thr | GTC Val | TCC Ser | TCA Ser 125 | | | | 375 | |
| (2) | INF | ORMA | TION | FOR | SEQ | ID | NO: | 38: | | | | | | | | | |

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 75

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 105

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 115

- (2) INFORMATION FOR SEQ ID NO: 39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: lymphocvyte
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-11
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number

40

Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp

35

S

70 65 Phe Ala Thr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe 90 85

Gly Gln Gly Thr Asn Leu Gln Ile Lys 100

- (2) INFORMATION FOR SEQ ID NO: 41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult

 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-14
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 14
 - (B) MAP POSITION: q32.3
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...375
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(91..105, 148..198, 295..342)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

| CAG Gln | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCT Ser | GGG Gly | GGA Gly | GGC Gly 10 | GTG Val | GTC Val | CAG Gln | CCG Pro | GGG Gly 15 | GGG Gly | 48 |
|------------|------------|------------|------------|-----------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|----|
|------------|------------|------------|------------|-----------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|----|

| TCC Ser | CTG Leu | AGA Arg | GTC Val | GCC Ala | TGT Cys | GTA Val | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | TTC Phe | AGG Arg 30 | AAT Asn | TTT Phe | 96 |
|------------|------------|------------|------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|----|
|------------|------------|------------|------------|------------|------------|------------|------------|------------------|------------|------------|------------|------------|------------------|------------|------------|----|

| 20 | | | | | |
|------------------------------------|----------------------------|----------------------------------|----------------------------------|----------------------------|------------|
| GGC ATG CAC TGG Gly Met His Trp | GTC CGC CAG Val Arg Gln | GCT CCA GGC Ala Pro Gly 40 | AAG GGG CTG Lys Gly Leu 45 | GAG TGG GTG Glu Trp Val | 3 144 1 |

GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT 192

| Ala | Phe 50 | Ile | Trp | Phe | Asp | Ala 55 | Ser | Asn | Lys | Gly | Tyr 60 | Gly | Asp | Ser | Val | | |
|------------------|------------|-------------------|-------------------|------------------|------------------|------------|-------------------|-------------------|------------------|------------------|------------|-------------------|-------------------|------------------|------------------|---|-----|
| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | GTC Val 70 | TCC Ser | AGA Arg | GAC Asp | AAT Asn | TCC Ser 75 | AAG Lys | AAC Asn | ACG Thr | CTC Leu | TAT Tyr 80 | 2 | 40 |
| CTG Leu | CAA Gln | ATG Met | AAC Asn | GGC Gly 85 | CTG Leu | AGA Arg | GCC Ala | GAA Glu | GAC Asp 90 | ACG Thr | GCT Ala | GTA Val | TAT Tyr | TAT Tyr 95 | TGT Cys | 2 | 88 |
| GCG Ala | AGA Arg | GAG Glu | AAG Lys 100 | GCG Ala | GTT Val | CGG Arg | GGA Gly | ATT Ile 105 | AGT Ser | AGA Arg | TAC Tyr | AAC Asn | TAC Tyr 110 | TAC Tyr | ATG Met | 3 | 336 |
| GAC Asp | GTC Val | TGG Trp 115 | GGC Gly | AAG Lys | GGG Gly | ACC Thr | ACG Thr 120 | GTC Val | ACC Thr | GTC Val | TCC Ser | TCA Ser 125 | | | | 3 | 375 |

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

| 3 | ` |
|---|---|
| G | 1 |

| . (1 | Lii) | нүрс | OTHE | CICAI | : NO |) | | | | | • | | | | | |
|------------------|------------------|------------------|-----------------------------------|----------------------------------|--------------------------------|----------------------------|-----------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| • (| (iv) | ANT: | I-SEN | 1SE: | NO | | | | | | | | | | | |
| | (v) | FRAG | GMEN? | г түі | PE: 1 | N-te | cmina | al | | | | | | | | |
| i | (vi) | (A (C (D | GINAI) ORC) INI) DE) HAI) CE | SANIS DIVII VELOI PLOT' | SM:] DUAL PMEN' YPE: | Homo ISO: TAL dip | LATE STAG: loid | : hy | peri: dult | mmun | e Rho | esus | D do | onor | | |
| (' | vii) | (A | EDIA') LI) CL | BRAR' | Y: c | DNA | libr | ary, | LD2 | | | | | | | |
| (v | iii) | (A (B |) MA | ROMO: P PO | SOME SITI | /SEG ON: | p11 | | romo num | | 2 | | | | | |
| | (ix) | (A | TURE) NA) LO) OT | ME/K | ON - 1 | 2.1 | 5 ION: | /pro | duct | = "I | mmun | oglo | buli | n, F | ab" | |
| | (ix) | / A | TURE) NA) LO | ME/K | EY: ON:j | CDR1 | , CD | R2, 96, | CDR3 | .162 | , 25 | 92 | 85) | | | |
| | (xi) | SEQ | UENC | E DE | SCRI | PTIC | N: S | EQ I | D NC | : 43 | : | | | | | |
| GTG Val 1 | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TCC Ser | CTG Leu | TCT Ser 10 | GCA Ala | TCT Ser | GTG Val | GGA Gly | GAC Asp 15 | AGA Arg | 48 |
| GTC Val | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AGC Ser | ATT Ile | ATC Ile | AAC Asn | AAT Asn 30 | TTA Leu | AAT Asn | 96 |
| TGG Trp | TAT Tyr | CAG Gln 35 | CAG Gln | AAA Lys | CCA Pro | GGC Gly | AAA Lys 40 | GCC Ala | CCT Pro | GAA Glu | CTC Leu | CTG Leu 45 | ATC Ile | TAT Tyr | GCT Ala | 144 |
| GCA Ala | TCC Ser 50 | AGT Ser | TTG Leu | CAA Gln | AGT Ser | GGG Gly 55 | GTC Val | CCT Pro | TCA Ser | AGG Arg | TTC Phe 60 | CGT Arg | GGC Gly | AGT Ser | GGA Gly | 192 |
| TCT Ser 65 | GGG Gly | AGA Arg | GAT Asp | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | GTC Val | ACC Thr | AGT Ser 75 | CTG Leu | CAA Gln | CCT Pro | GAA Glu | GAT Asp 80 | 240 |
| TTT Phe | GCA Ala | ACT Thr | TAC Tyr | TAC Tyr 85 | TGT Cys | CAA Gln | CAG Gln | AGT Ser | TAC Tyr 90 | Ser | ACC Thr | CTG Leu | TGG Trp | ACG Thr 95 | 1110 | 288 |
| GGC Gly | CAA Gln | GGG Gly | ACC Thr 100 | AAG Lys | GTG Val | GAA Glu | ATC Ile | AAA Lys 105 | • | | | | | | | 315 |
| (2) | INF | ORMA' | TION | FOR | SEQ | ID | NO: | 44: | | | | | | | | |

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala 35

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly

Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp 70

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe 90

Gly Gln Gly Thr Lys Val Glu Ile Lys

- (2) INFORMATION FOR SEQ ID NO: 45:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:

 - (A) ORGANISM: Homo sapiens(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA llibrary
 - (B) CLONE: LD2-17
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 14
 - (B) MAP POSITION: q32.43
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION:1..375
 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE:
 (A) NAME/KEY: CDR1, CDR2, CDR3

(B) LOCATION: join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

| | • | | | | | | | | | | | | | | | |
|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|
| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCT Ser | GGG Gly | GGA Gly | GGC Gly 10 | GTG Val | GTC Val | CAG Gln | CCG Pro | GGG Gly 15 | GGG Gly | 48 |
| TCC Ser | CTG Leu | AGA Arg | CTC Leu 20 | TCC Ser | TGT Cys | GTA Val | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | TTC Phe | AGG Arg 30 | AGT Ser | TAT Tyr | 96 |
| GGC Gly | ATG Met | CAC His | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCA Pro | GGC Gly | AAG Lys | GGC Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
| GCT Ala | TTT Phe 50 | ATA Ile | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | AGT Ser | AAT Asn | AAA Lys | GGA Gly | TAT Tyr 60 | GTA Val | GAC Asp | TCC Ser | GTG Val | 192 |
| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | ATC Ile 70 | TCC Ser | CGA Arg | GAC Asp | AAT Asn | TCC Ser 75 | AAG Lys | AAC Asn | ACG Thr | CTC Leu | TAT Tyr 80 | 240 |
| CTG Leu | CAA Gln | ATG Met | AAG Lys | AGC Ser 85 | CTG Leu | AGA Arg | GCC Ala | GAG Glu | GAC Asp 90 | ACG Thr | GCT Ala | GTA Val | TAT Tyr | TAT Tyr 95 | TGT Cys | 288 |
| GCG Ala | AGA Arg | GAG Glu | AAG Lys 100 | GCG Ala | CTT Leu | CGG Arg | GGA Gly | ATC Ile 105 | AGT Ser | AGA Arg | TAC Tyr | AAC Asn | TAT Tyr 110 | T X T | CTG Leu | 336 |
| GAC Asp | GTC Val | TGG Trp 115 | Gly | AAG Lys | GGG Gly | ACC Thr | ACG Thr 120 | Val | ACC Thr | GTC Val | TCC Ser | TCA Ser 125 | | | | 375 |

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60

| 65 | | | Phe | | 70 | | | | | • • | | | | | | |
|----------|------------|------------|--|--|--------------------------------|-------------------------------|--------------------------|---------------------|--------------------|--------------|--------------|------------|--------------|--------------------|--------------------|--------------|
| | | | Lys | 85 | | | | | , , | | | | | | | |
| Ala | Arg | Glu | Lys 100 | Ala | Leů | Arg | Gly | Ile 105 | Ser | Arg | Tyr | Asn | Tyr 110 | Tyr | Leu | |
| Asp | Val | Trp 115 | Gly | Lys | Gly | Thr | Thr 120 | Val | Thr | Val | Ser | Ser 125 | | | | |
| (2) | INF | ORMA | TION | FOR | SEQ | ID | ио: | 47: | | | | | | | | |
| | | (| QUEN A) L B) T C) S D) T | ENGT YPE: TRAN OPOL | H: 3 nuc DEDN OGY: | leic ESS: lin | ase aci sin ear | pair d gle | | | | | | | | |
| | (ii |) MC | LECU | LE T | YPE: | CDN | A to | mRN | IA | | | | | | | |
| | (iii | .) НУ | POTH | ETIC | AL: | ИО | | | | | | | | | | |
| | • | | TI-S | | | | | | | | | | | | | |
| | 7) | 7) FF | RAGME | ENT T | YPE: | N-t | erm: | inal | | | | | | | | |
| | · | , | RIGIN (A) (C) (C) (D) (E) (E) (C) (C) (C) | ORGAN ENDIV DEVEI HAPLO CELL | IISM: IDUA LOPMI TYPI | HOI AL IS ENTAS E: d | SOLA L ST iplo | re: AGE: id | adu. | IC | | | us D | don | or | |
| | (vi | | MMED: (A) : (B) : | LIBR | ARY: | CDN | A li 7 | brar | у, L | D2 | | | | | | |
| | (vii | i) P | OSIT (A) (B) (C) | CHRO | MOSO | ME/S TTON | EGME | . 1 | chro | | | | | | | |
| | (i | ж) F | | NAME | | | | ON:/E | produ | ıct= | "Imr | nunoç | globi | ılin | , Fak | o " |
| | (i | .x) F | EATU (A) (B) | | KEY TION | : CI I:jo: |)R1, in(6 | CDR2 | 2, CI 5, 1 | OR3 | 162, | 259 | 28 | 5) | | |
| | () | ci) S | SEQUI | ENCE | DESC | CRIP | rion | : SE | Q ID | NO: | 47: | | | | | |
| Va | il Me 1 | et Tl | nr G | ln Se | 5 P | ro P | ne s | er n | eu D | 10 | | | | | AC A sp A 15 | |
| GT Va | C A | CC A' | le T | CT TO hr Cy 20 | GC CO | GG G rg A | CA A la S | GT C er G | AG A ln A 25 | AC A sn I | TT A le A | GG A | GT T er P | TT I he I 30 | TA A Leu S | GT 96 Ser |

| TGG Trp | TAT Tyr | CAG Gln 35 | CAG Gln | AAA Lys | CCA Pro | GGG Gly | ACA Thr 40 | GCC Ala | CCT Pro | AAG Lys | CTC Leu | CTG Leu 45 | ATC Ile | TAT Tyr | GCT Ala | 14 | 4 |
|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------|------------------|------------------|----|----|
| GCA Ala | TCC Ser 50 | AGG Arg | TTG Leu | CAA Gln | AGT Ser | GGG Gly 55 | GTC Val | CCA Pro | TCA Ser | AGG Arg | TTC Phe 60 | AGT Ser | GGC Gly | AGT Ser | GGG Gly | 19 | 2 |
| TCT Ser 65 | GGG Gly | ACA Thr | GAT Asp | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | ATC Ile | AGC Ser | ACT Thr 75 | CTG Leu | CAA Gln | CCT Pro | GAA Glu | GAT Asp 80 | 24 | 0 |
| TTT Phe | GCG Ala | ACT Thr | TAC Tyr | TAC Tyr 85 | TGT Cys | CAA Gln | CAG Gln | AGT Ser | TAC Tyr 90 | AGT Ser | GCC Ala | CCT Pro | TGG Trp | ACG Thr 95 | TTC Phe | 28 | 8 |
| GGC Gly | CAA Gln | GGG Gly | ACC Thr 100 | AAG Lys | CTG Leu | GAA Glu | ATC Ile | AAA Lys 105 | | | | | | | | 31 | .5 |

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
- Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15
- Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser 20 25 30
- Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
- Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
- Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 65 70 75 80
- Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 85 90 95
- Gly Gln Gly Thr Lys Leu Glu Ile Lys 100 105

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO

| (| (iv) | ANT | I-SE | NSE: | МО | | | | | | | | | | | |
|------------------|-------------------|----------------|----------------------|---------------------------------|--------------------------------|----------------------------|-----------------------|-------------------|------------------|------------------|-------------------|------------|-------------------|------------------|------------------|-----|
| | (v) | FRA | GMEN' | r TY | PE: 1 | N-te | rmina | al | | | | | | | | |
| 1 | (vi) | (A (C (D |) DE | GANI: DIVI: VELO: PLOT | SM: I DUAL PMEN' YPE: | Homo ISO: TAL dip | LATE STAG: loid | : hy E: a | peri | | | esus | D do | onor | | |
| (| vii) | (A | EDIA) LI) CL | BRAR | Y: c | DNA | libr | ary | LD2 | | | | | | | · |
| (v: | iii) | (A |) MA | ROMO P PO | SOME SITI | /SEG ON: | q32. | 3 | romo | | 14 | | | | | |
| | (ix) | (A | TURE) NA) LO) OT | ME/K | ON: 1 | 37 | 5 ION: | /pro | duct | = "I | mmun | oglo | buli | n, F | ab" | |
| | (ix) | (A | TURE) NA) LO | ME/K | EY: ON:j | CDR1 oin(| , CD 91 | R2, 105, | CDR3 | 19 | 8, 2 | 95 | 342) | | | |
| | (xi) | SEÇ | UENC | E DE | SCRI | PTIC | N: S | EQ I | D NO | : 49 | : | | | | | |
| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCT Ser | GGG Gly | GGA Gly | GGC Gly 10 | GTG Val | GTC Val | CAG Gln | CCG Pro | GGG Gly 15 | GGG Gly | 48 |
| TCC Ser | CTG Leu | AGA Arg | CTC Leu 20 | TCC Ser | TGT Cys | GTA Val | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | TCC Ser | AGG Arg 30 | AGT Ser | TAT Tyr | 96 |
| GGC Gly | ATG Met 50 | CAC His | TGG Trp | GTC Val | CGC Arg | CAG Gln 55 | GCT Ala | CCA Pro | GGC Gly | AAG Lys | GGC Gly 60 | CTG Leu | GAG Glu | TGG Trp | GTG Val | 144 |
| GCT Ala 65 | TTT Phe | ATA Ile | TGG Trp | TTT Phe | GAT Asp 70 | GGA Gly | AGT Ser | AAT Asn | AAA Lys | GGA Gly 75 | TAT Tyr | GTA Val | GAC Asp | TCC Ser | GTG Val 80 | 192 |
| AAG Lys | GGC Gly | CGA Arg | TTC Phe | ACC Thr 85 | ATC Ile | TCC Ser | CGA Arg | GAC Asp | AAT Asn 90 | TCC Ser | AAG Lys | AAC Asn | ACG Thr | CTC Leu 95 | TAT Tyr | 240 |
| CTG Leu | CAA Gln | ATG Met | AAG Lys 100 | AGC Ser | CTG Leu | AGA Arg | GCC Ala | GAG Glu 105 | GAC Asp | ACG Thr | GCT Ala | GTA Val | TAT Tyr 110 | TAT Tyr | TGT Cys | 288 |
| GCG Ala | AGA Arg | GAG Glu | AAG Lys 205 | GCG Ala | CTT Leu | CGG Arg | GGA Gly | ATC Ile 210 | AGT Ser | AGA Arg | TAC Tyr | AAC Asn | TAT Tyr 215 | TÄT | CTG Leu | 336 |
| GAC Asp | GTC Val 115 | TGG Trp | GGC Gly | AAG Lys | GGG Gly | ACC Thr 120 | Thr | GTC Val | ACC | GTC Val | TCC Ser 125 | Ser | | | | 375 |

- (2) INFORMATION FOR SEQ ID NO: 50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120

- (2) INFORMATION FOR SEQ ID NO: 51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD2
 - (B) CLONE: LD2-20
 - (viii) POSITION IN GENOME:

| | | í B |) MA | P PO | SOME SITI Chr | ON: | p11 | | | | 2 | | | | | |
|------------------|------------------|------------------|------------------------|------------------|----------------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| | (ix) | (A | i T.O | ME/K | EY: ON:1 INFO | 31 | 5 ION: | /pro | duct | := "I | mmun | oglo | buli | n, F | ab" | |
| | (ix) | (2 | TURE () NA () LC | ME/K | ŒY: ON:j | CDR1 | , CD | R2, 96, | CDR3 | .162 | 2, 25 | 92 | 85) | | | |
| | (xi) | SEÇ | OUENC | E DE | ESCRI | PTIC | N: S | EQ I | D NC | 51 | . : | | | | | |
| GTG Val | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TCC Ser | CTG Leu | TCT Ser 10 | GCA Ala | TCT Ser | GTA Val | GGA Gly | GAC Asp 15 | AGA Arg | 48 |
| GTC Val | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AGC Ser | ATT Ile | AGC Ser | AGC Ser | TAT Tyr 30 | TTA Leu | AAT Asn | 96 |
| TGG Trp | TAT | CAG Gln 35 | CAG Gln | AAA Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AAG Lys | CTC Leu | CTG Leu 45 | ATC Ile | TAT Tyr | GCT Ala | 144 |
| GCA Ala | TCC Ser 50 | AGT Ser | TTG Leu | CAA Gln | AGT Ser | GGG Gly 55 | GTC Val | CCA Pro | TCA Ser | AGG Arg | TTC Phe 60 | AGT Ser | GGC Gly | AGT Ser | GGA Gly | 192 |
| TCT Ser 65 | GGG Gly | ACA Thr | GAT Asp | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | ATC Ile | AGC Ser | AGT Ser 75 | Leu | CAA Gln | CCT Pro | GAA Glu | GAT Asp 80 | 240 |
| TTT Phe | GCA Ala | ACT Thr | TAC Tyr | TAC Tyr 85 | Cys | CAA Gln | CAG Gln | AGT Ser | TAC Tyr 90 | Ser | ACC Thr | CGA Arg | TTC Phe | ACT Thr 95 | TTC Phe | 288 |
| GG(| C CCT | GGG Gly | ACC Thr 100 | Lys | GTG Val | GAT Asp | ATC Ile | AAA Lys 105 | | | | | | | | 315 |
| (2) | INF | | | | | | | | | | | | | | | |
| | | (| A) L B) T | ENGT YPE: | CHA H: 1 ami OGY: | 05 a no a | mino cid | TICS aci | : ds | | | | | | | |
| | (ii (xi |) MO | LECU QUEN | LE T | YPE: ESCR | pro IPTI | tein | SEQ | ID N | io: 5 | 2: | | | | | |
| ; | 1 | | | 5 | | | | | 10 | , | | | | 1- | | |
| Va. | l Thr | Ile | Thr 20 | | Arg | Ala | Ser | Glr 25 | ser | : Ile | e Ser | Ser | Туг 30 | Leu) | a Asn | |
| Tr | р Туг | Gln 35 | | Lys | Pro | Glý | Lys 40 | Ala | Pro | Lys | s Lev | Leu 45 | ı Ile | э Туг | Ala | |

| Ala | Ser 50 | Ser | Leu | Gln | Ser | Gly 55 | Val | Pro | Ser | Arg | Phe 60 | Ser | Gly | Ser | Gly | |
|-----------------|------------|------------------|---------------------------------|--|--------------------------------|-----------------------------|---------------------|------------------|--------------|------------|------------|------------|------------|------------|------------|----|
| Ser 65 | Gly | Thr | Asp | Phe | Thr 70 | Leu | Thr | Ile | Ser | Ser 75 | Leu | Gln | Pro | Glu | Asp 80 | |
| Phe | Ala | Thr | Tyr | Tyr 85 | Cys | Gln | Gln | Ser | Tyr 90 | Ser | Thr | Arg | Phe | Thr 95 | Phe | |
| Gly | Pro | Gly | Thr 100 | Lys | Val | Asp | Ile | Lys 105 | | | | | | | | |
| (2) | INFO | ORMAT | rion | FOR | SEQ | ID 1 | 10: | 53: | | | | | | | | • |
| | (i) | (<i>I</i> (I | A) LI B) T' C) S' | CE CHENGTHE PROPERTY OF COLUMN THE COLUMN TH | i: 38 nuci DEDNI | 34 ba Leic ESS: | ase pacionsing | pair: 1 | S | | | | | | | |
| | (ii) | MOI | LECU | LE T | YPE: | CDN | A to | mRN | A | | | | | | | |
| | (iii) | НУІ | POTH | ETIC | AL: 1 | 10 | | | | | | | | | | |
| | (iv) |) ANT | ri-si | ENSE | : NO | | | | | | | | | | | |
| | (v) |) FR | AGME | NT T | YPE: | N-t | ermi | nal | | | | | | | | |
| | (vi) | (2 (0 (1 | A) 01 C) II D) D: E) H | AL SORGANI NDIVI EVELO APLO ELL | ISM: IDUA: OPME: IYPE | Hom L IS NTAL : di | OLAT STA ploi | E: h GE: d | yper adul | t | | | s D | dono | r | |
| | (vii) | (2 | A) L | ATE : IBRAI LONE | RY: | CDNA | lib 17 | rary | , LD | 1 | | | | | | |
| (, | viii | (2 | A) C | ON II HROM AP P NITS | OSOM OSIT | E/SE ION: | GMEN q32 | . 3 | | | | | | | | |
| | (ix | (2 | B) T | AME/I | TON: | 13 | 84 | :/pr | oduc | :t= " | Immu | ınogl | .obul | .in, | Fab" | |
| | (ix | C | ATUR A) N B) L | E: AME/ OCAT | KEY: ION: | CDR join | 1, C (91. | DR2, | CDR | 3 81 | .98, | 295. | .351 | .) | | |
| | (xi |) SE | QUEN | CE D | ESCR | IPTI | on: | SEQ | ID N | 10: 5 | 3: | | | | | |
| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | Glu | TCI Ser | GGG Gly | GGA Gly | GGC Gly | val | GTC Val | CAC Glr | CCI Pro | GGG Gly | AGG Arg | 48 |
| TCC Ser | CTG Leu | AGA Arg | CTT Leu | TCC Ser | TGT Cys | GCA Ala | GCG | TCI Ser | GGA Gly | TTI Phe | ACC Thr | TTC Phe | AGT Sei | AGC Sei | TAT | 96 |

| Gly | ATG Met | CAC His 35 | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCA Pro | GGC Gly | AAG Lys | GGG Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|
| GCA Ala | GAT Asp 50 | ATA Ile | TGG Trp | TTT Phe | GAT Asp | GGA Gly 55 | GGT Gly | AAT Asn | AAA Lys | CAT His | TAT Tyr 60 | GCA Ala | GAC Asp | TTC Phe | GTG Val | 192 |
| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | ATC Ile 70 | TCC Ser | AGA Arg | GAC Asp | AAT Asn | TCC Ser 75 | AAG Lys | AAC Asn | ACG Thr | GTG Val | TAT Tyr 80 | 240 |
| CTA Leu | CAA Gln | ATG Met | AAC Asn | AGC Ser 85 | CTG Leu | AGA Arg | GTC Val | GAG Glu | GAC Asp 90 | ACG Thr | GCT Ala | GTG Val | TAT Tyr | TAC Tyr 95 | TGT Cys | 288 |
| GCG Ala | AGG Arg | GAT Asp | TAC Tyr 100 | TAT Tyr | AGC Ser | GTT Val | ACT Thr | AAG Lys 105 | AAA Lys | CTC Leu | AGA Arg | CTC Leu | CAC His 110 | TYL | TAC Tyr | 336 |
| TAC Tyr | TAC Tyr | ATG Met 220 | GAC Asp | GTC Val | TGG Trp | GGC Gly | AAA Lys 225 | GGG Gly | ACC Thr | ACG Thr | GTC Val | ACC Thr 230 | vai | TCC Ser | TCA Ser | 384 |

46

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val 50 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 100 105 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 315 base pairs

| (| (ii) | MOLI | ECULI | TYF | PE: C | DNA | to m | IRNA | | | | | | | | | |
|-----------------|------------|-------------------|------------------|--|--------------------------------|-----------------------------|------------------------|------------------|------------------|------------|------------|------------------|------------------|------------------|------------|----|----|
| (: | Lii) | нүрс | OTHE | CICAI | . NC | | | | | | | | | | | | |
| | (iv) | ANT | I-SEI | NSE: | NO | | | | | | | | | | | | |
| | (v) | FRAC | GMEN' | r TYI | PE: 1 | 1-tei | cmina | al | | | | | | | | | |
| | (vi) | (A) (C) (D) | ORG | L SOU GANIS DIVII VELOI PLOT LL T | SM: H DUAL PMENT VPE: | IOMO ISO IAL S dip | LATE: STAGI loid | : hyp | dult | | | esus | D do | onor | | · | |
| (| vii) | (A |) LI | TE SOBRARY | Y: cl | DNA . | libra 7 | ary, | LD1 | | | | | | | | |
| (v | iii) | (A |) CH | N IN ROMO: P PO: ITS: | SOME SITI | /SEG | p11 | | | | 2 | | | | | | |
| | (ix) | (A | · • | : ME/K CATI HER | ONT . 1 | 21 | 5 ION: | /pro | duct | = "I | mmun | oglo | buli | n, F | ab" | | |
| | | (A (B |) LO | ME/K CATI | on:j | oin(| 64 | 96, | 142. | .162 | | 92 | 85) | | | | |
| | • | | | E DE | | | | | | | | cm3 | cc. | CAC | 7 C 7 | 4 | 8 |
| GTG Val 1 | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TCC Ser | CTG Leu | TCT Ser 10 | GCA Ala | Ser | Val | GGA | Asp 15 | Arg | - | • |
| GTC Val | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | GGC Gly | ATT Ile | AGA Arg | AAT Asn | GAT Asp 30 | TTA Leu | ACC Thr | 9 | 6 |
| TGG Trp | TAT Tyr | CAG Gln 35 | CAA Gln | AAA Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AAG Lys | CTC Leu | CTG Leu 45 | ATC Ile | TAT Tyr | GCT Ala | 14 | 4 |
| Ala | Ser 50 | Asn | Leu | CAA Gln | Ser | 55 | Val | Pro | Ser | Arg | 60 | Der | Gly | 501 | 3-1 | 19 | |
| Ser 65 | Gly | Thr | Asp | TTC Phe | Thr 70 | Leu | Thr | 11e | Ser | 75 | Deu | G11 | 110 | 024 | 80 | 24 | |
| TTT Phe | GCA Ala | ACT Thr | TAT Tyr | TAC Tyr 85 | TGT Cys | CTA Leu | CAA Gln | GAT Asp | AAC Asn 90 | ASII | TTC Phe | CCG Pro | TAC Tyr | ACT Thr 95 | | 28 | 38 |
| | | | | | | | | | | | | | | | | | |

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

GGC CAG GGG ACC AAG CTG GAG ATC AAA Gly Gln Gly Thr Lys Leu Glu Ile Lys 100

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala

Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65

Phe Ala Thr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe

Gly Gln Gly Thr Lys Leu Glu Ile Lys

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library, LD1 and LD2
- (B) CLONE: LD1/2-6-3

(viii) POSITION IN GENOME:

| | (ix) | (A | I) LC | ME/F | CEY: CON:1 | 37 | 5 LION: | /pro | duct | := "I | mmur | noglo | buli | .n, F | 'ab" | |
|------------------|------------------|-------------------|------------------------|------------------|----------------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-----|
| | (ix) | (2 | TURE 1) NA 3) LO | ME/E | KEY: | CDR1 | , CI 91 | R2, 105, | CDR3 | 3 319 | 98, 2 | 295 | 342) | | | |
| | (xi) | SEÇ | QUENC | E DI | ESCRI | PTIC | on: S | SEQ 1 | D NO |): 57 | 7: | | | | | |
| CAG Gln 1 | GTG Val | AAA Lys | CTG Leu | CTC Leu 5 | GAG Glu | TCT Ser | GGG Gly | GGA Gly | GGC Gly 10 | GTG Val | GTC Val | CAG Gln | CCG Pro | GGG Gly 15 | GGG Gly | 48 |
| TCC Ser | CTG Leu | AGA Arg | GTC Val 20 | GCC Ala | TGT Cys | GTA Val | GCG Ala | TCT Ser 25 | GGA Gly | TTC Phe | ACC Thr | TTC Phe | AGG Arg 30 | AAT Asn | TTT Phe | 96 |
| GGC Gly | ATG Met | CAC His 35 | TGG Trp | GTC Val | CGC Arg | CAG Gln | GCT Ala 40 | CCA Pro | GGC Gly | AAG Lys | GGG Gly | CTG Leu 45 | GAG Glu | TGG Trp | GTG Val | 144 |
| GCT Ala | TTT Phe 50 | ATT Ile | TGG Trp | TTT Phe | GAT Asp | GCA Ala 55 | AGT Ser | AAT Asn | AAA Lys | GGA Gly | TAT Tyr 60 | GGA Gly | GAC Asp | TCC Ser | GTT Val | 192 |
| AAG Lys 65 | GGC Gly | CGA Arg | TTC Phe | ACC Thr | GTC Val 70 | TCC Ser | AGA Arg | GAC Asp | AAT Asn | TCC Ser 75 | AAG Lys | AAC Asn | ACG Thr | CTC Leu | TAT Tyr 80 | 240 |
| CTG Leu | CAA Gln | ATG Met | AAC Asn | GGC Gly 85 | CTG Leu | AGA Arg | GCC Ala | GAA Glu | GAC Asp 90 | ACG Thr | GCT Ala | GTA Val | TAT Tyr | TAT Tyr 95 | TGT Cys | 288 |
| GCG Ala | AGA Arg | GAG Glu | AAG Lys 100 | GCG Ala | GTT Val | CGG Arg | GGA Gly | ATT Ile 105 | Ser | AGA Arg | TAC Tyr | AAC Asn | TAC Tyr 110 | TAC Tyr | ATG Met | 336 |
| GAC Asp | GTC Val | TGG Trp 115 | GGC Gly | AAG Lys | GGG Gly | ACC Thr | ACG Thr 120 | Val | ACC Thr | GTC Val | TCC Ser | TCA Ser 125 | | | | 375 |
| (2) | INF | OR MA ' | TION | FOR | SEQ | ID | NO: | 58: | | | | | | | | |
| | | (, | A) L B) T | ENGT YPE: | CHA H: 1 ami OGY: | 25 a no a | mino cid | TICS aci | : ds | | | | | | | |
| | (ii (xi |) MO | LECU QUEN | LE T | YPE: ESCR | pro IPTI | tein ON: | SEQ | ID N | o: 5 | 8: | | | | | |
| 1 | | | | 5 | 1 | | | | 10 | • | | | | 1. | | |
| Ser | Leu | Arg | Val 20 | | Cys | Val | Ala | Ser 25 | Gly | Phe | Thr | Phe | Arg |)) | Phe | |

(A) CHROMOSOME/SEGMENT: chromosome 14(B) MAP POSITION: q32.3(C) UNITS: Chromosome band number

ily Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

la Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 50 55

ys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD1 and LD2
 - (B) CLONE: LD1/2-6-3
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 2
 - (B) MAP POSITION: p11
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..315
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION: join(64..96, 142..162, 259..285)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

| TG /al i | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TCC Ser | CTG Leu | TCT Ser 10 | GCA Ala | TCT Ser | GTA Val | GGA Gly | GAC Asp 15 | AGA Arg | 48 |
|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| TC Val | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AGC Ser | ATT Ile | ATC Ile | AGA Arg | TAT Tyr 30 | TTA Leu | AAT Asn | 96 |
| rgg Irp | TAT Tyr | CAG Gln 35 | CAC His | AAA Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AAG Lys | CTC Leu | CTG Leu 45 | ATC Ile | CAT His | ACT Thr | 144 |
| GCA Ala | TCC Ser 50 | AGT Ser | TTG Leu | CAA Gln | AGT Ser | GGG Gly 55 | GTC Val | CCG Pro | TCA Ser | AGG Arg | TTC Phe 60 | AGT Ser | GGC Gly | AGT Ser | GTA Val | 192 |
| TCT Ser 65 | GGG Gly | ACA Thr | GAT Asp | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | ATC Ile | AGC Ser | AGT Ser 75 | CTG Leu | CAA Gln | CCT Pro | GAA Glu | GAT Asp 80 | 240 |
| TTT Phe | GCA Ala | ACT Thr | TAC Tyr | TAC Tyr 85 | TGT Cys | CAA Gln | CAG Gln | AGT Ser | TAC Tyr 90 | ACT Thr | ACC | CCG Pro | TAC Tyr | ACT Thr 95 | TTT Phe | 288 |
| GGC Gly | CAG Gln | GGG Gly | ACC Thr 100 | Lys | CTG Leu | CAG Gln | ATC Ile | AAA Lys 105 | | | | | | | | 315 |
| (2) | TNF | ORMA | TION | FOR | SEQ | ID | NO: | 60: | | | | | | | | |

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr 35

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val 55

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 75 70 65

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe 95 90

Gly Gln Gly Thr Lys Leu Gln Ile Lys 105 100

- (2) INFORMATION FOR SEQ ID NO: 61:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs

| • | • | (C | TYI STI | RANDI | EDNE | ss: s | sing: | le | | | | | | | | |
|---|--|--|--|---|--|--|---|--|---------------------------------|--|--|--|--|--|--|-------------------------|
| | (ii) | MOLECULE TYPE: cDNA to mRNA | | | | | | | | | | | | | | |
| (| iii) | НУР | HYPOTHETICAL: NO | | | | | | | | | | | | | |
| | (iv) | ANT | ANTI-SENSE: NO | | | | | | | | | | | | | |
| | (v) | FRAGMENT TYPE: N-terminal | | | | | | | | | | | | | | |
| | (vi) | ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesud D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B | | | | | | | | | | | | | | |
| (| vii) | (A | EDIA) LI) CL | BRAR | Y: c | DNA | libr -33 | ary, | LD1 | and | LD2 | | | | | |
| (v | iii) | (A | ITIO) CH) MA) UN | ROMO P PO | SOME SITI | /SEG ON: | q32. | 3 | | | 14 | | | | | |
| | (ix) | ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" | | | | | | | | | | | | | | |
| (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91105, 148198, 295342) | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | 342) | | | |
| | | | UENC | E DE | SCRI | PTIC | N: 5 | SEQ I | D NC |): 61 | . : | | | | ccc | 49 |
| CAG Gln 1 | CITIC | *** | | E DE | SCRI | PTIC | N: S | SEQ I | D NO |): 61 GTG | .: GTC | CAG | CCG | GGG | GGG Gly | 48 |
| 3ln 1 | GTG Val | AAA Lys | UENC | CTC Leu 5 | SCRI GAG Glu TGT | TCT Ser | GGG Gly GCG | SEQ I GGA Gly TCT | GGC Gly 10 | GTG Val | GTC Val | CAG Gln TTC | CCG Pro | GGG Gly 15 | TTT | 48 96 |
| 3ln 1 rcc ser | GTG Val CTG Leu | AAA Lys AGA Arg | CTG Leu GTC Val | CTC Ala | GAG Glu TGT Cys | TCT Ser GTA Val | GGG Gly GCG Ala | GGA Gly TCT Ser 25 | GGC GGC | GTG Val TTC Phe | GTC Val ACC Thr | CAG Gln TTC Phe | CCG Pro AGG Arg 30 | GGG Gly 15 AAT Asn | TTT Phe | |
| 3ln 1 rcc ser GGC Gly | GTG Val CTG Leu ATG Met | AAA Lys AGA Arg CAC His 35 | CTG Leu GTC Val 20 | CTC Leu 5 GCC Ala GTC Val | GAG Glu TGT Cys CGC Arg | TCT Ser GTA Val CAG Gln | GGG Gly GCG Ala GCT Ala 40 | GGA Gly TCT Ser 25 CCA Pro | GGC Gly GGA Gly GGC Gly | GTG Val TTC Phe AAG Lys | GTC Val ACC Thr GGG Gly | CAG Gln TTC Phe CTG Leu 45 | CCG Pro AGG Arg 30 GAG Glu | GGG Gly 15 AAT ASN TGG Trp | TTT Phe GTG Val | 96 |
| In 1 ICC Ser GGC Gly GCT Ala | GTG Val CTG Leu ATG Met | AAA Lys AGA Arg CAC His 35 ATT Ile | CTG Leu GTC Val 20 TGG Trp | CTC Leu 5 GCC Ala GTC Val | GAG Glu TGT Cys CGC Arg GAT Asp | TCT Ser GTA Val CAG Gln GCA Ala 55 | GGG Gly GCG Ala GCT Ala 40 AGT Ser | GGA Gly TCT Ser 25 CCA Pro AAT Asn | GGC Gly GGC Gly AAA Lys | GTG Val TTC Phe AAG Lys GGA Gly | GTC Val ACC Thr GGG Gly TAT Tyr 60 AAG | CAG Gln TTC Phe CTG Leu 45 GGA Gly | CCG Pro AGG Arg 30 GAG Glu GAC Asp | GGG Gly 15 AAT Asn TGG Trp TCC Ser | TTT Phe GTG Val GTT Val | 96 144 192 240 |
| In 1 ICC Ser GGC Gly GCT Ala AAG Lys 65 | GTG Val CTG Leu ATG Met TTT Phe 50 GGC Gly | AAA Lys AGA Arg CAC His 35 ATT Ile CGA Arg | CTG Leu GTC Val 20 TGG Trp TGG Trp | CTC Leu 5 GCC Ala GTC Val TTT Phe ACC Thr | GAG GAU TGT Cys CGC Arg GAT Asp GTC Val 70 | TCT Ser GTA Val CAG Gln GCA Ala 55 TCC Ser | GCC GGG GGG GCG Ala GCT Ala 40 AGT Ser | GEQ I GGA Gly TCT Ser 25 CCA Pro AAT Asn GAC Asp | GGC Gly GGA Gly AAA Lys AAT Asn | GTG Val TTC Phe AAG Lys GGA Gly TCC Ser 75 | GTC Val ACC Thr GGG Gly TAT Tyr 60 AAG Lys | CAG Gln TTC Phe CTG Leu 45 GGA Gly AAC Asn | CCG Pro AGG Arg 30 GAG Glu GAC Asp ACG Thr | GGG Gly 15 AAT Asn TGG Trp TCC Ser CTC Leu | TTT Phe GTG Val GTT Val TAT Tyr 80 TGT Cys | 96 144 192 |

100 105

TCA

AC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCA Sp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115

375

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

In Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 20 25 30

Fly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Resus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid

| | , 17 | (G |) CE | LL T | YPE: | Per | Tbue | Lai | тушр | HOCY | CE D | | | | | |
|--|------------------|---|-------------------|----------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|-----|
| γ | vii) | (A |) LI | TE S BRAR ONE: | Y: c | DNA | libr -33 | ary, | LD1 | and | LD2 | | | | | |
| (v | iii) | POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number | | | | | | | | | | | | | | |
| | (ix) | FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" | | | | | | | | | | | | | | |
| | (ix) |) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285) | | | | | | | | | | | | | | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63: | | | | | | | | | | | | | | | | |
| TG al | ATG Met | ACC Thr | CAG Gln | TCT Ser 5 | CCA Pro | TCC Ser | TTC Phe | CTG Leu | TCT Ser 10 | GCA Ala | TCT Ser | GTA Val | GGA Gly | GAC Asp 15 | AGA Arg | 48 |
| TC al | ACC Thr | ATC Ile | ACT Thr 20 | TGC Cys | CGG Arg | GCA Ala | AGT Ser | CAG Gln 25 | AGC Ser | ATT Ile | ATC Ile | AGA Arg | TAT Tyr 30 | TTA Leu | AAT Asn | 96 |
| :GG :rp | TAT Tyr | CAG Gln 35 | CAC His | AAA Lys | CCA Pro | GGG Gly | AAA Lys 40 | GCC Ala | CCT Pro | AAG Lys | CTC Leu | CTG Leu 45 | ATC Ile | CAT His | GCT Ala | 144 |
| ;CA | TCC Ser 50 | AGT Ser | TTG Leu | CAA Gln | AGT Ser | GGG Gly 55 | GTC Val | CCG Pro | TCA Ser | AGG Arg | TTC Phe 60 | AGT Ser | GGC Gly | AGT Ser | GTA Val | 192 |
| CT Ser 65 | GGG Gly | ACA Thr | GAT Asp | TTC Phe | ACT Thr 70 | CTC Leu | ACC Thr | ATC Ile | AGC Ser | AGT Ser 75 | CTG Leu | CAA Gln | CCT Pro | GAA Glu | GAT Asp 80 | 240 |
| ľTT ?he | GCA Ala | ACT Thr | TAC Tyr | TAC Tyr 85 | TGT Cys | CAA Gln | CAG Gln | AGT Ser | TAC Tyr 90 | Tnr | ACC Thr | CCG Pro | TAC Tyr | ACT Thr 95 | TTT Phe | 288 |
| 3GC 31y | CAG Gln | GGG Gly | ACC Thr 100 | AAG Lys | CTG Leu | CAG Gln | ATC Ile | AAA Lys 105 | | | | | | | | 315 |
| (2) | INF | ORMA | TION | FOR | SEQ | ID | NO: | 64: | | | | | | | | |
| (2) INFORMATION FOR SEQ ID NO: 64: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear | | | | | | | | | | | | | | | | |
| | (ii (xi |) MO | LECU | LE T | YPE: ESCR | pro IPTI | tein | SEQ | ID N | 10: 6 | 54: | | | | | |
| Val | | Thr | Gln | Ser 5 | Pro | Ser | Phe | . Lev | Ser 10 | Ala | Ser | · Val | Gly | Asp 15 | Arg | |

Val Thr Ile Thr 20 Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Leu Ile His Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 Phe Ala Thr Tyr Tyr Cys Gln Gln Gln Ser Tyr Thr Phe 95